

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 23, 1999, 23:01:47 ; Search time 360.53 Seconds
(without alignments)
1506.258 Million cell updates/sec

Title: US-09-205-015-3

Perfect score: 356

Sequence: 1 tcgacctctggaaacatc.....atctggagctgaagaattc 356

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database :

EST:*

- 1: em_est1:*
- 2: em_est2:*
- 3: em_est3:*
- 4: em_est4:*
- 5: em_est5:*
- 6: em_est6:*
- 7: em_est7:*
- 8: em_est8:*
- 9: em_est9:*
- 10: gb_est1:*
- 11: gb_est2:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: gb_est6:*
- 16: gb_est7:*
- 17: gb_est8:*
- 18: gb_est9:*
- 19: gb_est10:*
- 20: gb_est11:*
- 21: gb_est12:*
- 22: gb_est13:*
- 23: gb_est14:*
- 24: gb_est15:*
- 25: gb_est16:*
- 26: gb_est17:*
- 27: gb_est18:*
- 28: gb_est19:*
- 29: gb_est20:*
- 30: gb_est21:*
- 31: gb_est22:*
- 32: gb_est23:*
- 33: gb_est24:*
- 34: gb_est25:*
- 35: gb_est26:*
- 36: gb_est27:*
- 37: gb_est28:*
- 38: gb_est29:*
- 39: gb_est30:*
- 40: gb_est31:*
- 41: gb_est32:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	36.4	10.2	539 10	R18712 yf98f07.r1
2	35.2	9.9	895 26	AA788958 ag40d08.s

3	34.2	9.6	371 10	R26937	R26937 yh51b07.r1
c 4	33.6	9.4	324 10	R51962	R51962 y17h02.r1
5	33.6	9.4	506 14	AA083476	AA083476 zn32d08.s
c 6	33.6	9.4	361 18	AA373695	AA373695 ES85742
7	33.6	9.4	387 23	AI200590	AI200590 qf99c04.x
8	33.6	9.4	401 23	AI247873	AI247873 qh58c12.x
9	33.6	9.4	405 23	AI248529	AI248529 qh76h12.x
10	33.6	9.4	376 25	AA676940	AA676940 zj69g05.s
11	33.6	9.4	388 25	AA701392	AA701392 z167e04.s
12	33.6	9.4	413 29	AI049954	AI049954 an34h12.x
13	33.6	9.4	417 29	AI087130	AI087130 oz75c04.x
14	33.6	9.4	353 29	RIC00677A	DI5464 Rice cDNA,
15	33.6	9.4	394 30	AI050745	AI050745 ox94c10.s
16	33.6	9.4	388 30	AI080585	AI080585 oz67f07.x
17	33.6	9.4	450 30	AI086664	AI086664 oz57b11.x
18	33.6	9.4	436 30	AI086938	AI086938 oz70g07.x
19	33.6	9.4	406 31	AI167997	AI167997 oz88g09.x
20	33.4	9.4	582 12	N20987	N20987 yx57f01.s1
21	33.4	9.4	357 30	AI056745	AI056745 oy98e06.x
22	33.2	9.3	443 17	HSPD04245	F19640 H. sapiens E
23	32.8	9.2	237 13	W99245	W99245 mf60f04.r1
24	32.8	9.2	554 15	AA081405	AA081405 zn34g11.s
c 25	32.6	9.2	337 17	AA303662	AA303662 EST16334
c 26	32.2	9.0	467 10	T97491	T97491 yx53f10.r1
27	32	9.0	385 12	N21587	N21587 yx60g03.s1
28	32	9.0	586 15	AA155782	AA155782 zo49e10.s
c 29	32	9.0	432 19	AA130208	AA130208 z137d12.r
30	32	9.0	521 19	AA133991	AA133991 z137d12.s
31	32	9.0	497 30	AI095618	AI095618 qb24d04.x
32	31.8	8.9	606 12	N31902	N31902 yv21c09.s1
33	31.8	8.9	423 14	W51911	W51911 zc37f07.s1
34	31.8	8.9	425 20	AA462732	AA462732 vf91a07.r
35	31.8	8.9	583 21	AA521429	AA521429 aa69b07.s
36	31.8	8.9	500 31	AI184318	AI184318 qd39d12.x
37	31.6	8.9	549 15	AA147860	AA147860 zo50h09.s
38	31.6	8.9	427 24	AA423951	AA423951 zv79f12.r
39	31.4	8.8	459 12	N24635	N24635 yx89c12.s1
40	31.2	8.8	599 13	W22385	W22385 66G3 Human
41	31.2	8.8	396 27	AA187138	AA187138 zp62b08.s
c 42	31	8.7	477 13	N43182	N43182 EST51124 WA
43	31	8.7	427 22	AA565918	AA565918 nj31g04.s
c 44	31	8.7	465 26	AA776725	AA776725 ah49e04.s
c 45	30.8	8.7	556 31	C98110	C98110 Oryza sativ

ALIGNMENTS

RESULT 1

LOCUS	539 bp	mRNA	EST	14-APR-1995
DEFINITION	yf98f07.r1 Homo sapiens cDNA clone 30551 5' similar to SP:MEC2_RAT			
ACCESSION	R18712			
NID	9772322			
KEYWORDS	EST.			
SOURCE	human clone-30551 library-Soares infant brain lNIB vector-Lafmid BA			

host-DH10B (ampicillin resistant) primer-M13RPI Rsite1-Not I
Rsite2-Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGGAAGAAATTCGCGCGAGCAATTTTTTTTTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldi.

ORGANISM	Homo sapiens
REFERENCE	Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 539) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Contact: Wilson AN
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Insert size: 1.0 kb; Uni-ZAP XR vector; ~3' adaptor

sequence: 5' GAATTCGCCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTCTTTTCTTTTCTTTT 3'
/db_xref="taxon:9606"
/clone="549135"
/clone_lib="Stratagene endothelial cell 937223"
/dev_stage="umbilical vein, 1 passage"
/lab_host="SOLR (kanamycin resistant)"
complement(<1..>506)

BASE COUNT 135 a 123 c 124 g 123 t 1 others
ORIGIN

Query Match 9.4%; Score 33.6; DB 14; Length 506;
Best Local Similarity 48.0%; Pred. No. 4.3;
Matches 96; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 95 aaacacttgaggagacagataactgggccaaccatgactcagtccttcttgaggccaaca 154

Db 163 AAAAATAAAGGAAGCAGAAATCTGCTCAATGAGTAACAAGTCACCTACACATCCAAA 222

QY 155 ggactcttgatcctctgtgggtgaggtgggacaagggaaagggtgaatggtact 214

Db 223 TAACCATGCACACTGTTCTCTGGGAGGAGATGCCAGGCGAGAGTGGGCCACAT 282

QY 215 gctgattacaacctgtgtgctccctccctctgttattctgagagggagccatgc 274

Db 283 GATGGGGACATTCACCTCTGACCTCAGCACCCCTGTACTGGGGGGTGGCCAGTG 342

QY 275 ccaagtggttcacagccagg 294

Db 343 CCACAGTGGACTCTGAGATG 362

RESULT 6
AA373695/c 361 bp mRNA EST 21-APR-1997
LOCUS
DEFINITION ESF85742 HSC172 cells I Homo sapiens cDNA 5' end similar to
plasminogen activator inhibitor, type 1, endothelial, mRNA
sequence.

ACCESSION AA373695

NID g2026015

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;

Homo.

REFERENCE 1 (bases 1 to 361)

AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

Bult C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

White O., Sutton G., Blake J.A., Brandon R.C., Man-Wai C.,

Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,

Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghagen N.S.,

Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkie P.S.Jr.,

Kelley J.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M.,

Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,

Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R.,

Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y.,

Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J.,

Dimke D., Feng D.-F., Ferrie A., Fischer C., Hastings G.A.,

He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K.,

Kozak D.L., Kunsch C., Hungjun J., Li H., Weissner P.S., Olsen H.,

Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.M.,

Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C.,

Fraser C.M. and Venter J.C.

TITLE Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other_ESTs: THC165970

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse

Location/Qualifiers

1..361

/organism="Homo sapiens"

/note="Organ: lung; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

/db_xref="ATCC (inhost):178068"

/db_xref="taxon:9606"

/clone_lib="HSC172 cells I"

/cell_type="fibroblast"

/cell_line="HSC172 (16PDL)"

/dev_stage="fetal"

<1..>361

BASE COUNT 81 a 85 c 86 g 106 t 3 others

ORIGIN

Query Match 9.4%; Score 33.6; DB 18; Length 361;

Best Local Similarity 48.0%; Pred. No. 4.1; Indels 0; Gaps 0;

Matches 96; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 95 aaacacttgaggagacagataactgggccaaccatgactcagtccttcttgaggccaaca 154

Db 208 AAAAATAAAGGAAGCAGAAATCTGCTCAATGAGTAACAAGTCACCTACACATCCAAA 149

QY 155 ggactcttgatcctctgtgggtgaggtgggacaagggaaagggtgaatggtact 214

Db 148 TAACCATGCACACTGTTCTCTGGGAGGAGATGCCAGGCGAGAGTGGGCCACAT 89

QY 215 gctgattacaacctgtgtgctccctccctctgttattctgagagggagccatgc 274

Db 88 GATGGGGACATTCACCTCTGACCTCAGCACCCCTGTACTGGGGGGTGGCCAGTG 29

QY 275 ccaagtggttcacagccagg 294

Db 28 CCACAGTGGACTCTGAGATG 9

RESULT 7

AA373695/c 387 bp mRNA EST 29-NOV-1998

LOCUS

DEFINITION qf99c04.x1 Soares_placenta_8to9weeks_2NDHP8to9W Homo sapiens cDNA

clone IMAGE:1758150 3', mRNA sequence.

ACCESSION AI200590

NID g3753196

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 387)

AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 949 Std Error: 0.00

Seq primer: -40Up from Gibco

High quality sequence stop: 386.

Location/Qualifiers

1..387

FEATURES

liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAGAAATTAATAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

```
/db_xref="taxon:9606"  
/clone="460184"  
/clone_lib="Soares fetal liver spleen INFLS S1"  
/sex="male"  
/dev_stage="20 week-post conception fetus"  
/lab_host="n410B (ampicillin resistant)"
```

	Query Match	9.4%	Score 33.6;	DB 25;	Length 376;
	Best Local Similarity	48.0%;	Pred. NO. 4.2;		
	Matches 96;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
QY	95	aaacacttgaggagcagataactggggcccaaccactgactcagtgcttcttgaggggccaaca	154		
Db	160	AAAAATAAAGGAGCAGAAATCTGCTTCAATGAGTAAACAAGTACACCTACACTCCAAA	219		
QY	155	ggaactcttgagtcactcctgtgggggtggaggtggggacaaggaaagggtgaatggtact	214		
Db	220	TAACCCATGCACACTGTTTCTGGGGGGGAGATGGCCAGCCAGAGAGTGGGCCACAT	279		
QY	215	gctgattacaacctgtggtgctgctcccccctcctgttatctgagaggggaaggccatgc	274		
Db	280	GATGGGGGACATTCACTCTGCCACTGCAGCACCCTGTACTGGGGAGGGGTGGCCAGTG	339		
QY	275	ccaaactgttcacagccagg	294		

RESULT	11
AA701392	
LOCUS	388 bp mRNA EST 19-DEC-1997
DEFINITION	zif7e04.s1 Soares fetal liver spleen INFLS S1 Homo sapiens CDNA clone 435870 3', mRNA sequence.
ACCESSION	AA701392
NID	AA701392
KEYWORDS	EST.
SOURCE	92704557 human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 388)
AUTHORS	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krisman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 379.
Location/Qualifiers
1..388
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)


```

Primer [5']
TGTTCACCACTGAGTGGAGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_lib="Soares_senescent_fibroblasts_NBHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 107 a 103 c 99 g 108 t
ORIGIN

Query Match 9.4%; Score 33.6; DB 29; Length 417;
Best Local Similarity 48.0%; Pred. No. 4.2;
Matches 96; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 95 aaacacttgaggagcagtaactgcccacacatgactcgtcttcttgaggccaca 154
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 168 AAAAATAAAGGAAGCAGAAATCTGCTCAATGAGTAACACAGTCACCTACACTCCAAA 227
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 155 ggaacttcagtcactcgtgggtgggtgggtgggtgggtgggtgggtgggtgact 214
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 TAACCATGACACACTGTTCTGGGAGGAGGATGCGCAGGCGAGAGTGGGCCACAT 287
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 215 gctgattacaacctggtgctgcctccctcctctgttatctgagaggagccatgc 274
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 GATGGGGGACATTCACCTGCCACTGACAGCACCCTGACTGCTGGGGAGGGTGGCCAGTG 347
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 275 ccaaatgtttcacagccag 294
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 348 CCACAGTGGACTGTGAGATG 367
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
R1CC0677A 353 bp mRNA EST 15-JUL-1998
LOCUS
DEFINITION
Rice cDNA, partial sequence (C0677A), mRNA sequence.
ACCESSION
D15464
NID
9286657
KEYWORDS
EST; EST (expressed sequence tag).
SOURCE
Oryza sativa (strain:Nipponbare) callus cDNA to mRNA.
ORGANISM
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
REFERENCE
1 (sites)
Sasaki,T., Song,J., Koga-Ban,Y., Matsui,E., Fang,F., Higo,H.,
Nagasaki,H., Hori,M., Miya,M., Murayama-Kavano,E. et.al.
Toward cataloging all rice genes: large-scale sequencing of
randomly chosen rice cDNAs from a callus cDNA library
Plant J 6 (4), 615-624 (1994)
JOURNAL
95078950
MEDLINE
2 (bases 1 to 353)
REFERENCE
Sasaki,T. and Minobe,Y.
Rice cDNA from callus
JOURNAL
Unpublished (1993)
REFERENCE
3 (bases 1 to 353)
AUTHORS
Sasaki,T.
TITLE
Direct Submission
JOURNAL
Submitted (14-APR-1993) to the DDBJ/EMBL/GenBank databases. Takuji
Sasaki, National Institute of Agrobiological Resources, Rice Genome
Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp. Tel:0298-38-7441.
Fax:0298-38-7468)
PROJECT = "RGP".
COMMENT Location/Qualifiers
FEATURES
source
1..353
/organism="Oryza sativa"

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/strain="Nipponbare"
/db_xref="taxon:4530"
/tissue_type="callus"
BASE COUNT 64 a 62 c 138 g 88 t 1 others
ORIGIN

Query Match 9.4%; Score 33.6; DB 29; Length 353;
Best Local Similarity 48.9%; Pred. No. 4.1;
Matches 90; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 26 ccacagtccagcagcagcacatctcccaagcagaggtgagcagcatcagctgg 85
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 CCATGCCGCAAGGTACTAGATATGCTAGCGCCGAGGTGGCGGTAGTGGAGGGGAG 143
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 86 ggtctgtgaaacacttgaggagcagataactggggccacacatgactcagtcctcttg 145
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 GTGGTGGAGGGTCCGAGGATGGTTCTGGATGGGATCCGGCTCTGGCTCTGGGTATGGTC 203
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 146 agccaacagagactctgagtcactcctggtgggtgagtgagtgagacaggaagggtg 205
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 AGCCCGCGGATCTTCCGGTGGAGCATATGCTAGTGGAGCGGGGAGGTCAAGGTGGTG 263
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 206 atg 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 GAGG 267
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
A1050745 394 bp mRNA EST 24-SEP-1998
LOCUS
DEFINITION
clone IMAGE:1663986 3', mRNA sequence.
ACCESSION
A1050745
NID
93307550
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 394)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL
Tumor Gene Index
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 992 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 386.
Location/Qualifiers
1..394
/organism="Homo sapiens"
/notice="Vector: p773D (Pharmacia) with a modified
polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTCACCACTGAGTGGAGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_lib="Soares_senescent_fibroblasts_NBHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"

```


BASE COUNT	105 a	91 c	93 g	105 t
ORIGIN				

[illegible]

Search completed: June 23, 1999, 23:01:51
Job time: 1635 sec

